GenCore version  $5.1.4\_p5\_4578$  Copyright (c) 1993 - 2003 Compugen Ltd.

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AR028694 Sequence
AR028695 Sequence
AR028696 Sequence
AR086505 Sequence
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AR086509 Sequence
AR028699 Sequence
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## ALIGNMENTS

RESULT 1 AR028693/c

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	Sequence 9 from patent US 5858753.		AR028693.1 GI:5940666				ěď.	1 (bases 1 to 26)	1., Hoekstra	Se.	Patent: US 5858753-A 9 12-JAN-1999;	Location/Qualifiers
AR028693	Sednence 9	AR028693	AR028693.1		Unknown.	Unknown.	Unclassified.	1 (bases 1	Chantry, D. H	Lipid kinase	Patent: US	ង
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Chantry,D.H., Hoekstra,M.F. and Holtzman,D.A.
Lipid kinase
Lipid stent: US 8858753-A 11 12-JAN-1999;
                                                                                                     Chantry, D.H., Hoekstra, M.F. and Holtzman, D.A. Lipid kinase Patent: US 5985589-A 10 16-NOV-1999; Location/Qualifiers
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Sequence 11 from patent US 5858753.
AR028695.1 GI:5940668
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AR028696
AR028696.1 GI:5940669
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1 (bases 1 to 26)
Chantry, D.H., Hoekstra, M.F. and Holtzman, D.A.
Lipid kinase
Patent: US 5985589-A 9 16-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 25)
Chantry,D.H., Hoekstra,M.F. and Holtzman,D.A.
Lipid kinase
Patent: US 5858753-A 10 12-JAN-1999;
Location/Qualifiers
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Sequence 9 from patent US 5985589.
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AR086504.1 GI:10013270
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Patent: US 5858753-A 7 12-JAN-1999;
Location/Qualifiers
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1 (bases 1 to 22)
Chantry, D. H., Hoekstra, M. F. and Holtzman, D. A.
Lipid kinase
Patent: US 5858753-A 14 12-JAN-1999;
Location/Qualifiers
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Chantry,D.H., Hoekstra,M.F. and Holtzman,D.A.
Lipid kinase
Patent: US 5985589-A 14 16-NOV-1999;
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    Sequence 14 from patent US 5858753. AR028698.1 GI:5940671
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Chantry, D.H., Hoekstra, M.F. and Holtzman, D.A.
Lipid kinase
Patent: US 5985589-A 12 16-NOV-1999;
Location/Qualifiers
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Chantry,D.H., Hoekstra,M.F. and Holtzman,D.A.
Libid kinase,
Patent: US 5985589-A 11 16-NOV-1999;
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Unclassified.
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Job time : 32020 secs
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Chantry, D.H., Hoekstra, M.F. and Holtzman, D.A.
Lipid kinase
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Chantry, D. H., Hoekstra, M.F. and Holtzman, D.A.
Lipid Kinase
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Location/Qualifiers
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AR028692
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Universities 1 to 21)
Chantry,D.H., Hoekstra,M.F. and Holtzman,D.A.
Lipid kinase
Patent: US 5985589-A 8 16-NOV-1999;
Location/Qualifiers
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Sequence 8 from patent US 5985589.
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                                                                     GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

5 Description	Phosphatidylinosit	PCR primer used to	Human PI 3-kinase-	Phosphatidylinosit	PCR primer used to	Human PI 3-kinase-	Phosphatidylinosit	Phosphatidylinosit	Probe used to isol
SUMMARIES	AAV31345	AAX15937	AAZ32887	AAV31346	AAX15938	AAZ32888	AAV31347	AAV31348	AAX15939
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å Query Match	0.7	0.7	0.7	9.0	9.0	9.0	9.0	9.0	9.0
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Human PI 3-Kinase- Human PI 3-Kinase- Human PI 3-Kinase- Phosphatidylinosit PCR primer used to POLYMOCPHIC fragme Phosphatidylinosit Phosphatidylinosit Phosphatidylinosit PCR primer used to PCR primer us	MENTS elta subunit RACE primer. delta; human; immune system; er; RACE; ss.  DA;  talytic subunit - used to ise activity in immune system
AAX15540 AAX32889 AAX32889 AAX32889 AAX32889 AAX32882 AAX33343 AAX33343 AAX33343 AAX33343 AAX13156 AAX13118 AAX13120 AAX13121 AAX13121 AAX13122 AAX13123 AAX13128 AAX13128 AAX13128 AAX13128 AAX13128 AAX13128	ALIGN pll0 d pll0 d; pll0 R; prim ltzman ltzman
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Length 26; Indels

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immune system. pll0-delta phosphorylates phosphatidylinositol (PI), and derivatives of it at the 3'-hydroxyl of the inositol ring). pll0-delta may be used as an antigen in the production of antibodies (using standard techniques) which may be used, for example, to modulate (le blocking, inhibiting or stimulating) the binding between pll0-delta and its binding partner. pll0-delta may also be used in assays to identify modulators which inhibit or
                                                                                                                                                                                                                                                                                                                                                                                          Query Match 0.7%; Score 26; DB 20; I
Best Local Similarity 100.0%; Pred. No. 3.5e+04;
Matches 26; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                       Sequence 26 BP; 5 A; 8 C; 9 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1500 GGGAACGCTGCCTCTACATGTGGCCC 1525
                                                                                                                                                                                                                                                       activate its kinase activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
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                                                                                                                        2 Antisense gene-specific oligonucleotide primers (see AAV31345 and AAV31346) respectively comprise a primary RACE primer and a nested RACE primer, and are based on the 5' end of M#928, a cDNA clone obtained from human macrophage cDNA by PCR amplification (see AAV31343-44). They were used to amplify 5' sequences of human phosphatidylinostiol 3-kinase (PI 3-kinase) pl10 delta catalytic were used as templates in a nested PCR and the reamplified products were then analysed using probes (see AAV31347-48) specific for pl10 delta. The specific 5' RACE PCR products were combined with partial clones #349 and M#928 to produce a composite cDNA (AAV31340) sequence coding for human PI 3-kinase pl10 delta catalytic subinit (see AAW58570). This can be used to develop products for modulating and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PCR primers AAX15937-38 were used to isolate cDNA encoding a catalytic subunit (p110-delta), derived from a Phosphatidylinositol 3-kinase enzyme which is involved in PI3-Kinase mediated signalling in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel catalytic subunits derived from phosphatidylinositol 3-kinase enzymes - useful as antigens and for identifying agents which modulate the enzymes kinase activity or binding to substrates and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 26 BP; 5 A; 8 C; 9 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.7%; Score 26; DB 100.0%; Pred. No. 3.5 rative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1500 GGGAACGCTGCTCTACATGTGGCCC 1525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PI; kinase activity; PCR primēr; ss.
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                                                                   Example 1; Page 11; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           signalling and in carcinogenesis
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96US-0777405
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nes 26; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  carcinogenesis.
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Lipid kinase; catalytic; subunit; pl10-delta; PI 3-kinase; phosphorylation; phosphatidylinositol 3-kinase; heterodimeric; isoform; phosphorylation; phosphatidylinositol (3, 4, 5) triphosphate; PIP3; activation; G protein; cellular response; growth; differentiation; apoptosis; phosphorylated lipid; protein kinase C; PRC; leukocyte activation; interleukin-2; IL-2; production; T cell; leukocyte signalling; modulator; antagonist; treatment; disorder; cell growth; cell differentiation; immune activation; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence represents human pl10-delta PCR primer #9, used in the generation of a full-length cDNA (AA232882) encoding a novel lipid kinase catalytic subunit, pl10-delta, related to phosphatidylinositol 3-kinase (PI 3-kinase). PI 3-kinase is a heterodimer consisting of a membrane-localising p85 subunit and a catalytic pl10 subunit. These subunits both have isoforms; p85 has two isoforms (alpha and beta) which are differentially expressed, and pl10 has to date three isoforms (alpha, beta and gamma) that vary in their ability to associate with p85. PI 3-kinase phosphorylates PI and phosphorylated derivatives of PI at the 3' hydroxyl of the inositol ring with the primary product of PI 3-kinase-mediated phosphorylation being phosphatidinositol (3, 4, 5) triphosphate (PIP3). PI 3-kinase is activated by interaction with G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human PI 3-kinase-related catalytic subunit p110-delta PCR primer #9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identifying modulators of lipid kinase subunit pl10delta activity
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26 GGGAACGCTGCCTCTACATGTGGCCC 1
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AAZ32887 standard; DNA; 26 BP.
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25-NOV-1996;
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proteins and PI 3-kinase activation is believed to be involved in a prange of cellular responses including cell growth, differentiation and apoptosis. The downstream targets of the phosphorylated lipids generated following PI 3-kinase activation have not been well characterised, although some isoforms of protein kinase C (PKC) are directly activated by PIP3 in vitro. PI 3-kinase also appears to be involved in certain aspects of leukocyte activation, such as interleukin-2 (IL-2) production in T cells, and leukocyte signalling through G-protein coupled to identify modulators of pil0-delta and/or PI 3-kinase activity. These may be useful in the treatment of disorders associated with cell growth,
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AAV31345) respectively comprise a primary RACE primer and a nested
CAAV31345) respectively comprise a primary RACE primer and a nested
CAAV31343-44). They were used to amplify 5' sequences of human
CAAV31343-44). They were used to amplify 5' sequences of human
phosphatidylinostic) 3'kinase (PI 3'kinase) pl10 delta catalytic
CAAV31343-44). Single leucocyte cDNA as template. Amplified products
CAAV31343-44). While probes (see AAV31347-48) specific for pl10
CAAV31341 The specific 5' RACE PCR products were combined with
CAAV31340 partial clones #249 and M#928 to produce a composite cDNA (AAV31340)
CAAV31340 partial clones #249 and M#928 to produce a composite cDNA (AAV31340)
CAAV31340 partial clones #249 and M#928 to produce a composite cDNA (AAV31340)
CAAV31340 partial clones #249 and W#928 to produce a composite cDNA (AAV31340)
CAAV31340 partial clones #249 and W#928 to product a composite cDNA (AAV31340)
CAAV31340 partial clones #249 and W#928 to product a composite cDNA (AAV31340)
CAAV31340 partial clones #249 and W#928 to product a composite cDNA (AAV31340)
CAAV31340 partial clones #249 and W#928 to product a composite cDNA (AAV31340)
CAAV31340 partial clones #249 and W#928 to product a composite cDNA (AAV31340)
CAAV31340 partial clones #249 and W#928 to product a composite cDNA (AAV31340)
                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Phosphatidylinositol 3-kinase; pl10 delta; human; immune system; carcinogenesis; diagnosis; PCR; primer; RACE; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Phosphatidylinositol 3-kinase p110 delta subunit RACE primer.
                                                                                                                                                                                                                                                                                        Length 26;
                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                              cell differentiation, apoptosis or immune activation.
                                                                                                                                                                                                                                                                                  Query Match

0.7%; Score 26; DB 21; I
Best Local Similarity 100.0%; Pred. No. 3.5e+04;
Matches 26; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                   Sequence 26 BP; 5 A; 8 C; 9 G; 4 T; 0 other;
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AAV31346/C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Catalytic subunit; p110-delta; phosphatidylinositol 3-kinase; P13-Kinase mediated signalling; immune system; phosphatidylinositol; PI; kinase activity; PCR primer; ss.
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                                                                                                                                          Length 25;
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PI 3-kinase activity in immune system signalling and in carcinogenesis.
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0.6%; Score 25; DB 20; I
Best Local Similarity 100.0%; Pred. No. 5.6e+04;
Matches 25; Conservative 0; Mismatches 0;
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                                                                                                                                    Query Match
0.6%; Score 25; DB 19; I
Best Local Similarity 100.0%; Pred. No. 5.6e+04;
Matches 25; Conservative 0; Mismatches 0;
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                                                                                Sequence 25 BP; 4 A; 9 C; 10 G; 2 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Holtzman DA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Columns 6; 22pp; English.
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                                                                                                                                                                                                                                                     1435 GGCGGACTGCCCCATTGCCTGGGCC 1459
                                                                                                                                                                                                                                                                                  25 GGCGGACTGCCCCATTGCCTGGGCC 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP
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96US-0777405
                                                                                                                                                                                                                                                                                                                                                                                                                       AAX15938/c
ID AAX15938 standard; DNA; 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hoekstra MF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-MAY-1999 (first entry)
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25-NOV-1996;
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Gaps

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Indels

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Mismatches

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Conservative

25;

Matches

1459

g

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REBULT 6

AM222888 Standard; DNA; 25 BP.

AM222888; Standard; DNA; 25 BP.

AM222888; Standard; DNA; 25 BP.

AM222888; Standard; DNA; 25 BP.

Might Kinase; Catalytic; Subunit; Dillo-delta PCR Primar; Primar;
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Length 25;

0.6%; Score 25; DB 21; 1 100.0%; Pred. No. 5.6e+04;

Query Match Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 Oligonucleotide probes (see AAV31347 and AAV31348) are specific for the human phosphatidylinostiol 3-kinase (PI 3-kinase) pl10 delta catalytic subunit. They were used in Southern blotting to screen clones obtained from 5'RACE and nested PCR amplifications of human leukocyte cDNA (see AAV31345-46). Specific 5'RACE PCR products were identified, and were combined with partial clones #249 and M#928 to produce a composite cDNA (AAV31340) sequence coding for human PI 3-kinase pl10 delta catalytic subinit (see AAW58570). This can be used to develop products for modulating PI 3-kinase activity in immune system signalling and in carcinogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                 New phosphatidylinositol 3-kinase catalytic subunit - used to develop products for modulating kinase activity in immune system signalling and in carcinogenesis
                                                                                                                             Phosphatidylinositol 3-kinase; p110 delta; human; immune system; carcinogenesis; diagnosis; probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                 Phosphatidylinositol 3-kinase p110 delta subunit probe.
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0.6%; Score 23; DB 19; Le
Pred. No. 1.46+05;
0;
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                                                                                                                                                                                                                                                                                                                                                            Chantry DH, Hoekstra MF, Holtzman DA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Page 11; 53pp; English,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1149 CCCTGGAGCAGCGTTCCGCATC 1171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Pre-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23 CCCTGGAGCAGCCGTTCCGCATC
                                                                                                                                                                                                                                                                         97WO-US21655
AAV31347/c
ID AAV31347 standard; DNA; 23
                                                                                                                                                                                                                                                                                                     96US-0777405
                                                                      12-OCT-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAV31348 standard; DNA; 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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les 23; Conserv
                                                                                                                                                                                                                                                                                                                                (ICOS-) ICOS CORP.
                                                                                                                                                                      Synthetic.
Homo sapiens.
                                                                                                                                                                                                                W09823760-A1
                                                                                                                                                                                                                                                                       25-NOV-1997;
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                                                                                                                                                                                                                                            04-JUN-1998.
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                                           AAV31347;
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ID AAV3134
XX
AC AAV3134
XX
DT 12-OCT-
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Homo sapiens. WO9823760-A1 25-NOV-1997;

04-JUN-1998

25-NOV-1996;

Chantry DH,

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Catalytic subunit; pl10-delta; phosphatidylinositol 3-kinase; pl3-Kinase mediated signalling; immune system; phosphatidylinositol; PI; kinase activity; probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel catalytic subunits derived from phosphatidylinositol 3-kinase enzymes - useful as antigens and for identifying agents which
                                                                                                                                                                                                                                                                                                                                        subunit (pilo-delta), derived from a Phosphatidylinositol 3-Kinase enzyme which is involved in P13-Kinase mediated signalling in the immune system. pilo-delta phosphorylates phosphatidylinositol [P1], and derivatives of it at the 3'-hydroxyl of the inositol ring). pilo-delta may be used as an antigen in the production of antibodies (using standard techniques) which may be used, for example, to modulate (le blocking, inhibiting or stimulating) the binding between pilo-delta and its binding partner. pilo-delta may also be used in assays to identify modulators which inhibit or activate its kinase activity.
                                                                                                                                                                           Novel catalytic subunits derived from phosphatidylinositol 3-kinase enzymes - useful as antigens and for identifying agents which modulate the enzymes kinase activity or binding to substrates and
                                                                                                                                                                                                                                                                                                                           Probes AAX15939-40 were used to isolate cDNA encoding a catalytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Probe used to isolate cDNA sequence encoding pl10-delta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.6%; Score 23; DB 20; I
100.0%; Pred. No. 1.4e+05;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 23 BP; 4 A; 6 C; 10 G; 3 T; 0 other;
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                                                                                                      Holtzman DA;
                                                                                                                                                                                                                                                                                      Example 1; Columns 7; 22pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1149 CCCTGGAGCAGCCGTTCCGCATC 1171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23 CCCTGGAGCAGCCGTTCCGCATC 1
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96US-0777405.
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97US-0977871.
96US-0777405.
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                                                                                                      Hoekstra MF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 100.
hes 23; Conservative
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                                                              (ICOS-) ICOS CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-NOV-1997;
25-NOV-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-MAY-1999
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  25-NOV-1997;
25-NOV-1996;
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                                                                                                         Chantry DH,
                                                                                                                                                                                                                                                    co-factors
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 Oligonucleotide probes (see AAV31347 and AAV31348) are specific for the human phosphatidylinostiol 3-kinase (PI 3-kinase) pl10 delta catalytic subunit. They were used in Southern blotting to screen clones obtained from 5'RACE and nested PCR amplifications of human leukcoyte cDNA (see AAV31345-46). Specific 5'RACE PCR products were identified, and were combined with partial clones #249 and M#928 to produce a composite cDNA (AAV31340) sequence coding for human PI 3-kinase pl10 delta catalytic subinit (see AAW58570). This can be used to devalop products for modulating PI 3-kinase activity in immune system signalling and in carcinogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Catalytic subunit; pl10-delta; phosphatidylinositol 3-kinase; pl3-Kinase mediated signalling; immune system; phosphatidylinositol; PI; kinase activity; probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       New phosphatidylinositol 3-kinase catalytic subunit - used to develop products for modulating kinase activity in immune system signalling and in carcinogenesis
                                                 Phosphatidylinositol 3-kinase; p110 delta; human; immune system;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ő
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0.6%; Score 23; DB 19; Length zo,
nnn.0%; Pred. No. 1.4e+05;
nnn.0%; Pred. No. 1.4e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Probe used to isolate cDNA sequence encoding pl10-delta.
        Phosphatidylinositol 3-kinase p110 delta subunit probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 23 BP; 8 A; 7 C; 8 G; 0 U; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 0.6%; Score 23; DB Best Local Similarity 100.0%; Pred. No. 1.4 Best Local Similarity 100.0%; Mismatches 23; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                              Holtzman DA;
                                                                      carcinogenesis; diagnosis; probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Page 11; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1132 CTCTGTGTCCCTGTGGTCCCTGG 1154
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AAX15939/C
ID AAX15939 standard; DNA; 23 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97US-0977871
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                                                                                                                                                                                                                                                                                                                                                                              Hoekstra MF,
                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1998-322736/28.
                                                                                                                                                                                                                                                                                                                                      (ICOS-) ICOS CORP.
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25-NOV-1997;

Homo sapiens

Synthetic.

AAX15939;

õ g JS5882910-A 16-MAR-1999

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Gaps

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membrane-localising p85 subunit and a catalytic p110 subunit. These subunits both have isoforms; p85 has two isoforms (alpha and beta) which care differentially expressed, and p110 has to date three isoforms (alpha, beta and gamma) that vary in their ability to associate with p85. P13 *Klase phosphorylates P1 and phosphorylated derivatives of P1 at the 3' hydroxyl of the inositol ring with the primary product of P1 3. *Kinase mediated phosphorylation being phosphatidylinositol (3, 4, 5) triphosphate (PPP). P1 3.*Kinase is activated by interaction with G proteins and P1 3.*Kinase activation is believed to be involved in a range of cellular responses including cell growth, differentiation and a proteins and P1 3.*Kinase activation is believed to be involved in a range of cellular responses including cell growth, differentiation and approteis. The downstream targets of the phosphorylated lippids generated following P1 3.*Kinase activation have not been well characterised, although some isoforms of protein kinase C (PKC) are directly activated following P1 3.*Kinase also appears to be involved in certain aspects of leukocyte signalling through G-protein coupled colls. In T cells, and leukocyte signalling through G-protein coupled colls. In T cells, and leukocyte signalling through G-protein coupled colls. In the treatment of disorders associated with cell growth, associated with cell growth, associated with cell growth, associated with cell growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lipid kinase; catalytic; subunit; pl10-delta; pl 3-kinase; phosphorylation; phosphatidylinositol 3-kinase; heterodimeric; isoform; phosphorylation; phosphatidylinositol (3, 4, 5) triphosphate; plPB; activation; G protein; cellular response; growth; differentiation; apoptosis; phosphorylated lipid; protein kinase C; PRC; leukocyte activation; interleukin-2; LL-2; production; T cell; leukocyte signalling; modulator; antagonist; treatment; disorder; cell growth; cell differentiation; immune activation; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human PI 3-kinase-related catalytic subunit p110-delta PCR primer #12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   dentifying modulators of lipid kinase subunit pl10delta activity -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cell differentiation, apoptosis or immune activation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.6%; Score 23; DB 21; I
100.0%; Pred. No. 1.4e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 23 BP; 4 A; 6 C; 10 G; 3 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Column 7; 22pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1149 CCCTGGAGCAGCGGTTCCGCATC 1171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23 CCCTGGAGCAGCCGTTCCGCATC 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0225951.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       890/c
AAZ32890 standard; DNA; 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
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25-NOV-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAZ32890;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lipid kinase; catalytic; subunit; pl10-delta; PI 3-kinase; phosphatidylinositol 3-kinase; heterodimeric; isoform; phosphorylation; phosphatidylinositol 3-kinase; heterodimeric; isoform; phosphorylation; d. 4. 5) triphosphate; PIP3; activation; G protein; cellular response; growth; differentiation; apoptosis; phosphorylated lipid; protein kinase C; PRC; leukocyte activation; interleukin 2: IL-2; production; T cell; leukocyte signalling; modulator; antagonist; agonist; treatment; disorder; cell growth; cell differentiation; immune activation; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence represents human pll0-delta PCR primer #11, used in the generation of a full-length cDNA (AA23282) encoding a novel lipid kinase catalytic subunit, pll0-delta, related to phosphatidylinositol 3-kinase (PI 3-kinase). PI 3-kinase is a heterodimer consisting of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human PI 3-kinase-related catalytic subunit p110-delta PCR primer #11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                   Probes AAX15939-40 were used to isolate cDNA encoding a catalytic subunit (pl10-delta), derived from a Phosphatidylinositol 3-kinase enzyme which is involved in P13-Kinase mediated signalling in the immune system. pl10-delta phosphorylates phosphatidylinositol (PI), and derivatives of it at the 3'-hydroxyl of the inositol ring). pl10-delta may be used as an antigen in the production of antibodies (using standard techniques) which may be used, for example, to modulate (ie blocking, inhibiting or stimulating) the blinding between pl10-delta and its binding partner. pl10-delta may activate its kinase activity.
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     modulate the enzymes kinase activity or binding to substrates and
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100.0%; Pred. No. 1.4e+05;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 23 BP; 8 A; 7 C; 8 G; 0 U; 0 other;
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                                                                                       Example 1; Columns 7; 22pp; English
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960S-0777405
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25-NOV-1996;
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                                     co-factors
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contraction of a full-length CDNA (AA212882) encoding a novel lipid kinase catalytic subunit, pl10-delta, related to phosphatidylinositol 3 kinase (pr 13 kinase). Pl 3 kinase is a heterodimer consisting of a membrane-localising p85 subunit and a catalytic pl10 subunit. These subunits both have isoforms; p85 has two isoforms (alpha and beta) which are differentially expressed, and pl10 has to date three isoforms (alpha, beta and gamma) that vary in their ability to associate with p85. Pl 3 kinase phosphorylates PI and phosphorylated derivatives of PI at the inositol ring with the primary product of PI 3 kinase-mediated phosphorylation being which princated (3, 4, 5) triphosphate (PIP3). PI 3 kinase is activated by interaction with G proteins and PI 3 kinase activation is believed to be involved in a range of cellular responses including cell growth, differentiation and apoptosis. The downstream targets of the phosphorylated lipids generated following PI 3 kinase activation have not been well characterised, although some isoforms of protein kinase C (PKC) are directly activated by PIP3 in vitro. PI 3 kinase also appears to be involved in certain aspects of leukocyte activation, such as interleukin-2 (IL-2) production in the treatment of disorders associated with cell growth, cell in the treatment of disorders associated with cell growth, cell differentiation, anothers are immined activity. These may cell afferentiation anothers are immined activation and inferentiation.
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sequence represents human p110-delta PCR primer #12, used in the
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; Pred. No. 1.4e+05;
0; Mismatches 0;
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Best Local Similarity 100.0
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PCR primers AAX15941-42 were used to isolate cDNA encoding a catalytic subunit (pll0-delta), derived from a Phosphatidylinositol 3-kinase enzyme which is involved in P13-Kinase mediated signalling in the immune system. pll0-delta phosphorylates phosphatidylinositol (PI), and derivatives of it at the 3' hydroxyl of the inositol ring). pll0-delta may be used as an antigen in the production of antibodies (using standard techniques) which may be used, for example, to modulate (ie blocking, inhibiting or stimmlating) the binding between pll0-delta and its binding partner. pll0-delta may also be used in assays to identify modulators which inhibit or
                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Catalytic subunit; pl10-delta; phosphatidylinositol 3-kinase; Pl3-Kinase mediated signalling; immune system; phosphatidylinositol; PI; kinase activity; PCR primer; ss.
amplification of 5'RACE PCR products (see AAV31345-46) of human leukocyte cDNA. The 5' primer includes a 5' BamHI site and sequences that code for a FLAG peptide (see AAW58571) which is product was combined with restriction fragments of partial clones $1249 and #$928 to produce a full-length cDNA (see AAV31347) for the phosphatidylinositol 3'kinase (PI 3'kinase). This was incorporated into expression vector pcDNA3, and FLAG-tagged pl10 delta was expressed in transfected COS cells. pl10 delta can be used to system signalling and in carcinogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel catalytic subunits derived from phosphatidylinositol 3-kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           enzymes - useful as antigens and for identifying agents which modulate the enzymes kinase activity or binding to substrates and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCR primer used to amplify cDNA sequence encoding p110-delta.
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                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lipid kinase; catalytic; subunit; pll0-delta; pl 3-kinase; phosphorylation; phosphatidylinositol 3-kinase; heterodimeric; isoform; phosphorylation; phosphatidylinositol (3, 4, 5) triphosphate; PIP3; activation; G protein; cellular response; growth; differentiation; apoptosis; phosphorylated lipid; protein kinase C; PRC; leukocyte activation; interleukin-2; LL-2; production; T cell; leukocyte signalling; modulator; antagonist; treatment; disorder; cell growth; es.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human PI 3-kinase-related catalytic subunit p110-delta PCR primer #14.
                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identifying modulators of lipid kinase subunit pl10delta activity
                                                                                                                                                                                                          ;
                                                                                                                                     Length 22;
                                                                                                                                                                                                      0; Indels
                                                                                                                                 0.6%; Score 22; DB 20; I
100.0%; Pred. No. 2.2e+05;
vative 0; Mismatches 0;
                                                                Sequence 22 BP; 5 A; 7 C; 6 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hoekstra MF, Chantry DH;
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                                                                                                                                                                                                                                                                           1501 GGAACGCTGCCTCTACATGTGG 1522
                                                                                                                                                                                                                                                                                                                  22 GGAACGCTGCCTCTACATGTGG 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :892/c
AAZ32892 standard; DNA; 22 BP.
activate its kinase activity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-FEB-2000 (first entry)
                                                                                                                                                                                                          22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-012785/01.
                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ICOS-) ICOS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-NOV-1997;
25-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-JAN-1999;
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                                                                                                                                         Query Match
                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAZ3289272
AAZ389272
AAZ3289272
AAZ32892
AAZ3289272
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in T cells, and leukocyte signalling through G-protein coupled receptors. pll0-delta, or nucleotides encoding it, may be used to identify modulators of pll0-delta and/or pr 3-kinase activity. These may be useful in the treatment of disorders associated with cell growth, cell differentiation, apoptosis or immune activation.
                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                            ö
                                                                                                                                                                                            Length 22
                                                                                                                                                                                                                                          Indels
                                                                                                                                                                      0.6%; Score 22; DB 21; L4
100.0%; Pred. No. 2.2e+05;
....man+rches 0;
                                                                                                                                            Sequence 22 BP; 5 A; 7 C; 6 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: March 3, 2003, 20:12:24
Job time: 741 secs
                                                                                                                                                                                                                                                                                       1501 GGAACGCTGCCTCTACATGTGG 1522
                                                                                                                                                                                                                                                                                                                     22 GGAACGCTGCCTCTACATGTGG 1
                                                                                                                                                                                                                   Local Similarity -
                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                        Best Loca
Matches
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Scoring table:

Searched:

Database

Perfect score:

Sequence:

nucleic

Run on:

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Gaps
                sequence 11, Sequence 12, Sequence 13, Sequence 14, Sequence 16, Sequence 16, Sequence 17, Sequence 20, Sequence 21, Sequence 22, Sequence 23, Sequence 23, Sequence 24, Sequence 25, Sequence 27, Sequence 27, Sequence 26, Sequence 27, Seque
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.7%; Score 26; DB 2; Length 26; 100.0%; Pred. No. 2.4e+03; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun STREET: 6300 Sears Tower/233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/777,405A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Chantry, David
APPLICANT: Hoekstra, Merl F.
APPLICANT: Holtzman, Douglas A
TITLE OF INVENTION: No. 5858753el Lipid Kinase
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
US-09-357-070-10
US-09-357-070-11
US-09-357-070-12
US-09-357-070-13
US-09-357-070-14
US-09-357-070-15
US-09-357-070-16
US-09-357-070-18
US-09-357-070-19
US-09-357-070-20
US-09-357-070-20
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US-09-357-070-22
US-09-357-070-23
US-09-357-070-24
US-09-357-070-25
US-09-357-070-25
US-09-357-070-25
US-09-357-070-25
US-09-357-070-25
US-09-357-070-25
                                                                                                                                                                                                                                                                                                                                                          ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIPICATION: 435
CLASSIPICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: No. 5858753and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/33441
FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1500 GGGAACGCTGCCTCTACATGTGGCCC 1525
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                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 9, Application US/08777405A
; Patent No. 5858753
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (312) 474-6300
TELEPAX: (312) 474-6448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS: LENGTH: 26 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26; Conservative
   COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 6300 Sear CITY: Chicago STATE: Illinois COUNTRY: USA
     US-08-777-405A-9/c
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8786.857 Million cell updates/sec
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Sequence 8
Sequence 1
Sequence 7
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Sequence 8
Sequence 8
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Sequence 1
Sequence 1
Sequence 2
Sequence 3
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Sequence 3
Sequence 7
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Sequence
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                                                                                                                               March 3, 2003, 19:58:31; Search time 135 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                         GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-777-405A-9

US-08-977-871A-9

US-08-977-871A-10

US-08-977-405A-110

US-08-977-405A-111

US-08-977-405A-112

US-08-977-405A-112

US-08-977-405A-112

US-08-977-871A-112

US-08-977-871A-112

US-08-977-871A-14

US-08-977-871A-14

US-08-977-871A-14

US-08-977-871A-14

US-08-977-871A-16

US-08-977-405A-16

US-08-977-405A-16

US-08-977-871A-16

US-08-977-871A-16
                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-357-070-3
US-09-357-070-8
US-09-357-070-9
                                                                                                                                                                                                                                                                                                                             441362 segs, 153338381 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Listing first 45 summaries

    nucleic search, using sw model

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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0% Maximum Match 100%
                                                                                                                                                                                                   US-10-049-743-1
3868
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Match Length
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Length 26;
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STREET: 6300 Sears Tower/233 South Wacker Drive
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/225,951
FLING DATE:
CLASSIFICATION:
ATTORNEY/AGBNT INFORMATION:
NAME: No. 5985589and, Greta E.
REFERENCE/DOCKET NUMBER: 27866/33441
TELECOMMUNICATION INFORMATION:
TELEFHONE: (312) 474-6300
TELEFHORE: (312) 474-6448
TELERA: 25-3856
INPORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
WYDE: nucleic acid
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US-08-777-405A-10/C
Sequence 10, Application US/08777405A
Patent No. 5858753
GENERAL INFORMATION:
APPLICANT: Chantry, David
APPLICANT: Holtzman, Douglas A
TITLE OF INFORMIN: No. 5858753e1 Lipid Kinase
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/777,405A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 0.7%; Score 26; DB 2; Le Best Local Similarity 100.0%; Pred. No. 2.4e+03; Matches 26; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: No. 5868753and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 35,302
RELECOMMUNICATION INFORMATION:
TELEPOME : 312,474-0448
TELERA: 25-3856
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHRACTERISTICS:
LENGTH: 25 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26 GGGAACGCTGCTCTACATGTGGCCC 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY; linear
; MOLECULE TYPE: CDNA
US-09-225-951-9
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CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
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Sequence 9, Application US/08977871A

Sequence 9, Application US/08977871A

Sequence 9, Application US/08977871A

Sequence 9, Application:

Sequence 9, Application:

Sequence 9, Application:

Sequence 10.

Sequence 10
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STREET: 6300 Sears Tower/233 South Wacker Drive
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Le . 2.4e+03;
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Patent No. 598589
CENERAL INFORMATION:
APPLICANT: Chantry, David
APPLICANT: Holekstra, Merl F.
APPLICANT: Holtzman, Douglas A
TITLE OF INVENTION:
NUMBER OF INVENTION:
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5882910and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/33441
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-6448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: single
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/777,405
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US-08-977-871A-9
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US-09-225-951-9/c
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APPLICANT: Chantry, David
APPLICANT: Chantry, David
APPLICANT: Hoekstra, Merl F.
APPLICANT: Holtzman, Douglas A
TITLE OF INVENTION: No. 598589el Lipid Kinase
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall O'Toole Gerstein Murray & Borur
STREET: 6300 Sears Tower/233 South Wacker Drive
CITY: Chicago
STREET: Lilinois
                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/225,951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1435 GGCGGACTGCCCCATTGCCTGGGCC 1459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 11, Application US/08777405A Patent No. 5858753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: No. 598559and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/POCKET NUMBER: 27866
TELECOMMUNICATION INFORMATION:
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TELEFAX: (312) 474-6300
TELEX: 25-8866
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleic acid
EDNESS: single
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear; MOLECULE TYPE: CDNA US-09-225-951-10
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Matches 25; Conserva
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CITY: Chicago
STATE: Illinois
COUNTRY: USA
    Patent No. 5985589
GENERAL INFORMATION:
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US-08-777-405A-11/c
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                                                                                                                                        Length 25;
                                                                                                                                   Query Match 0.6%; Score 25; DB 2; Length 25; Best Local Similarity 100.0%; Pred. No. 4e+03; Matches 25; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                             Sequence 10, Application US/08977871A
Fatent No. 5882910
GENERAL INFORMATION:
APPLICANT: Chantry, David
APPLICANT: Hockstra, Merl F.
APPLICANT: Hockstra, Merl F.
APPLICANT: Hockstra, Morl F.
APPLICANT: Hockstra, Merl F.
APPLICANT: Hockstra, Merl F.
APPLICANT: Hockstra, Merl F.
APPLICANT: GOUGHOES: 17
CORRESSONDENCES: 17
CORRESPONDENCES: Marshall O'Toole Gerstein Murray & Borun STREET: 6300 Sears Tower/233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/977,871A FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: No. 5882010and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/33441
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEX: 25,3856
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
                                                                                                                                                                                                                             1435 GGGGACTGCCCCATTGCCTGGGCC 1459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 60606
COMPUTER REARABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER: 08/777,405
FILING DATE:
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US-09-225-951-10/c
; Sequence 10, Application US/09225951
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
TYPE: nucleic acid
STRANDEDNESS: single
                                          ; TOPOLOGY: linear; MOLECULE TYPE: CDNA US-08-777-405A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: CDNA
US-08-977-871A-10
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CITY: Chicago
STATE: Illinois
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                         RESULT 5
US-08-977-871A-10/c
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APPLICANT: Chantry, David
APPLICANT: Hockstra, Merl F.
APPLICANT: HOLZEMAN, DOUGLAS A
TITLE OF INVENTION: No. 5858753el Lipid Kinase
NUMBER OF SEQUENCES: 17
CORRESPONDENE ADDRESS:
ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun
STREET: 6300 Sears Tower/233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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27866/33441
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            Indels
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APPLICANT: Hockstra, Merl F.
APPLICANT: Hockstra, Merl F.
APPLICANT: Holtzman, Douglas A
TITLE OF INVENTION: No. 5882910el Lipid Kinase
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun
STREET: 6300 Sears Tower/233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION NUMBER: US/08/977,871A
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Patent No. 5882910
GENERAL INFORMATION:
APPLICANT: Chantry, David
APPLICANT: Hoekstra, Merl F.
APPLICANT: HOLIZMAN, DOUGlas A
TILLE OF INVENTION: No. 5882910el Lipid Kinase
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
          0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: NO. 5882910and, Greta E.
REGISTRATION NUMBER: 35.302
REFERENCE/DOCKET NUMBER: 27866/33441
                                                                                                                                                               US-08-977-871A-11/c

Sequence 11, Application US/08977871A

Patent No. 5882910

GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/777,405
                                               1132 CTCTGTGTCCCTGTGGTCCCTGG 1154
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                                                                      23 CTCTGTGTCCCTGTGGTCCCTGG 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                        STREET: 6300 SearCITY: Chicago
STATE: Illinois
COUNTRY: USA
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          23;
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          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun STREET: 6300 Sears Tower/233 South Wacker Drive CITY: Chicago STRTE: 111,1101s
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/777,405A
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Pred. No. 1.1e+04;
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Sequence 12, Application US/08777405A
Patent No. 5858733
Patent No. 5858733
Patent No. 5858739
PAPLICANT: Chantry, David
PAPLICANT: Holtzman, Douglas A
TITLE OF INVENTION: No. 5858753el Lipid Kinase
                                                                                                                                                                                                                                                                                                                                                                                   Query Match 0.6%; Score 23; DB Best Local Similarity 100.0%; Pred. No. 1.1 Matches 23; Conservative 0; Mismatches
                                                                                                 REFERENCE/DOCKET NUMBER: 27866/33441
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27866/33441
                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear MOLECULE TYPE: other nucleic acid US-08-777-405A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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MOLECULE TYPE: other nucleic acid
US-08-777-405A-12
FILING DALE.
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 5858753and, Greta E.
NAME: No. 7858753and, Greta E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIETCATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5858753and, Greta E.
REGISTRATION NUMBER: 35,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1149 CCCTGGAGCAGCCGTTCCGCATC 1171
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TELEFAX: 25-3856
TELEFAX: 25-3856
INPORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                       TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-6300
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 base pairs
TYPE: nucleic acid
STRANDENNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23 CCCTGGAGCAGCCGTTCCGCATC 1
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELERAX: (312) 474-6448
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100.0%;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun STREET: 6300 Sears Tower/233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/225,951
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.6%; Score 23; DB 2; Le
ilarity 100.0%; Pred. No. 1.1e+04;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 12, Application US/09225951
Patent No. 5985589
GENERAL INFORMATION:
APPLICANT: Chantry, David
APPLICANT: Hockstra, Merl F.
APPLICANT: Holtzman, Douglas A
TITLE OF INVENTION: No. 5985589el Lipid Kinase
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27866/33441
  REFERENCE/DOCKET NUMBER: 27866/33441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear; MOLECULE TYPE: other nucleic acid US-09-225-951-12
                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: other nucleic acid US-09-225-951-11
                                                                                                                                                                                                                                                                                                                                                                          1149 CCCTGGAGCAGCGTTCCGCATC 1171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: No. 5985589and, Greta E.
REGISTRATION NUMBER: 35,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1132 CTCTGTGTCCCTGTGGTCCCTGG 1154
               TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-6448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23 CTCTGTGTCCCTGTGGTCCCTGG 1
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-0448
TELEPAX: (312) 474-0448
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INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 base pairs
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EDNESS: single
                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 6300 Sean
CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best_Local Similarity
Matches 23; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-225-951-12/c
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COUNTRY: USA
5: Marshall O'Toole Gerstein Murray & Borun 6300 Sears Tower/233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/225,951
                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/977,871A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 0.6%; Score 23; DB 2; I Best Local Similarity 100.0%; Pred. No. 1.1e+04; Matches 23; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Chantry, David
APPLICANT: Hoekstra, Merl F.
APPLICANT: Holtzman, Douglas A
TITLE OF INVENTION: No. 5985589el Lipid Kinase
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: No. 5882010and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/33441
TELECOMMUNICATION INFORMATION:
TELEFAX: (312) 474-6300
TELEXX: (312) 474-6448
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/777,405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1132 CTCTGTGTCCCTGTGGTCCCTGG 1154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 11, Application US/09225951
; Patent No. 5985589
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: No. 5985589and, Greta
REGISTRATION NUMBER: 35,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23 CTCTGTGTCCCTGTGGTCCCTGG 1
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleic acid
EDNESS: single
                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                   CLTY: Chicago
STATE: Illinois
COUNTRY: HSA
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                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
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US-09-225-951-11/C
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  ADDRESSEE:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/977,871A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLGGY: linear MOLECULE TYPE: other nucleic acid US-08-977-871A-14
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Best Local Similarity 100.0
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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CITY: Chicago
STATE: Illinois
COUNTRY: USA
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US-09-225-951-14/c
                                                                                                          FILING DATE
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                     RESULT 13
US-08-777-405A-14/C

Sequence 14, Application US/08777405A

Patent No. 5889153

APPLICANT: Chantry, David

APPLICANT: Hockstra, Merl F;

APPLICANT: Holtzman, Douglas A

TITLE OF INVENTION: No. 5858753el Lipid Kinase

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS: 17

ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun

STREET: 6300 Sears Tower/233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 14
US-08-977-871A-14/c
; Sequence 14, Application US/08977871A
; Patent No. 588210
; GENERAL INFORMATION:
APPLICANT: Chantry, David
APPLICANT: Holtzman, Douglas A
TITLE OF INVENTION: No. 5882910e1 Lipid Kinase
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun
STREET: G100 Sears Tower/233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 22;
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APPLICATION NUMBER: US/08/777,405A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 0.6%; Score 22; DB Best Local Similarity 100.0%; Pred. No. 1.8 Matches 22; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DAIE:
CLASSIFICATION: 435
ATTORNEY/AGENT INNORMATION:
NAME: NO. 5858753and, Greta E.
REGISTRATION NUMBER: 35,302
                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
US-08-777-405A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1501 GGAACGCTGCCTCTACATGTGG 1522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22 GGAACGCTGCTCTACATGTGG 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Gaps
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Patent No. 5985589
GENERAL INFORMATION:
APPLICANT: Chantry, David
APPLICANT: Hockstra, Merl F.
APPLICANT: Holtzman, Douglas A
TITLE OF INVENTION: No. 5985589el Lipid Kinase
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun
STREET: 6300 Sears Tower/233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATIS: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE:
FLIGG DATE:
CLASSIFICATION:
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100.0%; Pred. No. 1.8e+04;
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CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
PREJECTATION NUMBER: 08/777,405
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: No. 5882910and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/33441
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECAX: (312) 474-0448
TELEEXX: 25,3856
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
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NAME: NO. 59858940, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/33441
TELECOMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELERX: (312) 474-6448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
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Search completed: March 4, 2003, 06:27:43 Job time : 136 secs

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Sequence 1, Appli
Sequence 379, Ap
Sequence 3789, Ap
Sequence 3780, Ap
Sequence 16, Appl
Sequence 16, Appl
Sequence 178, Ap
Sequence 395, Ap
Sequence 395, Ap
Sequence 4394, Ap
Sequence 4394, Ap
Sequence 12035, Ap
                                                                                           (without alignments)
2338.022 Million cell updates/sec
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                                                                              March 3, 2003, 20:00:22 ; Search time 1105 Seconds
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// Cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
// Cgn2_6/ptodata/2/pubpna/NSO6_PUBCOMB.seq:*
// Cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
// Cgn2_6/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
// Cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
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GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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0 US-09-996 606-4
0 US-09-866-108-3799
0 US-09-894-633A-20
0 US-09-894-633A-20
0 US-09-894-633A-20
0 US-09-804-177-160
0 US-09-866-108-3764
0 US-09-866-108-378
0 US-09-866-108-3945
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0 US-09-866-108-12894
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                                                                                                                                                                                                                              478924 seqs, 333959956 residues
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                                                                                                                                                                                                                                                                                                                                                                                Published_Applications_NA:*
                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                     nucleic - nucleic search, using sw model
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Match Length
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length: 30
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Perfect score:
Seguence:
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Maximum DB seq
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Sequence 1. Application US/09494438

Sequence 1. Application US/09494438

Patent No. US20020037504a1

SERENAL INFORMATION:
APPLICANT: ARAHIRA, WASAOMI

APPLICANT: ARAHIRA, WETHOD FOR PREPARING TEMPLATE DNA FROM PROCESSED

TITLE OF INVENTION: WEETHOD FOR WHICH IS FEASIBLE FOR AMPLIFICATION OF

TITLE OF INVENTION: DNA REGION BY PCR METHOD

TITLE OF INVENTION: DNA REGION BY PCR METHOD

CURRENT APPLICATION NUMBER: US/09/494,438

CURRENT FILING DATE: 2000-01-31

PRIOR FILING DATE: 1999-11-26

NUMBER OF SEQ ID NOS: 11

SEQ ID NO 1

SEQ ID NO 1

LENGTH: 30
Sequence 12944, A Sequence 12985, A Sequence 13772, A Sequence 19, Appl Sequence 19, Appl Sequence 45, Appl Sequence 3896, Ap Sequence 3898, Ap Sequence 3899, Ap Sequence 2, Appl Sequence 2, Appl Sequence 1, Appl Sequence 3760, Ap Sequence 3760, Ap Sequence 3761, Appl Sequence 3761, App
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Patent No. US20020127653A1
GENERAL INFORMATION:
RAPLICANT: SOPET, DANIEL R.
STEVEN STEVEN M.
TITLE OF INVENTION: HEMATOPOLETIC SIGNALING FACTOR
 US-09-866-108-12944

US-09-866-108-13772

US-09-866-108-13772

US-09-785-548-19

US-09-785-548-19

US-09-785-548-19

US-09-785-548-19

US-09-918-203-4

US-09-918-203-4

US-09-866-108-3898

US-09-866-108-3898

US-09-866-108-3899

US-09-866-108-3899

US-09-866-108-3899

US-09-866-108-3899

US-09-866-108-3899

US-09-865-108-3800

US-09-865-108-3900

US-09-852-000-4

US-09-852-000-4

US-09-852-000-5

US-09-852-000-5

US-09-852-000-5

US-09-852-000-5

US-09-852-000-5

US-09-756-095-2
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                                                                                                                                                                                                                                                                                                                 US-09-866-108-3760
US-09-866-108-3761
US-09-866-108-3762
US-09-866-108-3943
US-09-866-108-3944
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Best Local Similarity 82.1%;
Matches 23; Conservative C
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ORGANISM: Artificial Sequence
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     RESULT 1
US-09-494-438-1/C
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     FEATURE
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NESULT A PRESULT A PAPLICATION US/09866108

Sequence 3780, Application US/09866108

Sequence 3780, Application US/09866108

Sequence 3780, Application US/09866108

Sequence 3780, Application US/09866108

APPLICANT: UJ. Yinggang

APPLICANT: Hawke, David R.

APPLICANT: Hawke, David R.

APPLICANT: SHANK, David R.

TITLE REPRESUED IN HUMAN HEART AND MUSCLE

FILE REPRESUES. ADOUGL-7

CURRENT APPLICATION NUMBER: US/09/866,108

CURRENT APPLICATION NUMBER: US/09/866,108

CURRENT APPLICATION NUMBER: US/00/666

PRIOR APPLICATION NUMBER: US/00/00-65-26

PRIOR PILING DATE: 2001-01-04

PRIOR FILING DATE: 2000-09-27

PRIOR PILING DATE: 2001-01-03

PRIOR PAPLICATION NUMBER: PCT/US01/00666

PRIOR PLING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR PLING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR PLING DATE: 2001-01-30

PRIOR PRIOR PLING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 0.5%; Score 17.6; DB 10; Best Local Similarity 83.3%; Pred. No. 2.8e+05; Matches 20; Conservative 0; Mismatches 4;
       PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR PELING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PRIOR DATE: 2001-01-30
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 15752
SEQ ID NO 3779
LENGTH: 25
LENGTH: 25
LENGTH: 25
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CORGANISM: Homo sapiens
US-09-866-108-3779
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FATELL NO. SOCULOWERSONAL

APPLICANT: GU, Yizhong

APPLICANT: DI, Yongsang

APPLICANT: PENN, Sharron G.

APPLICANT: RANK, David K.

APPLICANT: RANK, David K.

APPLICANT: HANZEL, David K.

APPLICANT: SHANNON, MARK

TITLE OF INVENTION: WYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

CURRENT APPLICATION NUMBER: US/09/866,108

CURRENT PILING DATE: 2001-05-25

PRIOR FILING DATE: 2000-05-26

PRIOR PLILOR DATE: 2000-06-4

PRIOR PLILOR DATE: 2000-06-4

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR PLILNG DATE: 2001-09-37

PRIOR PLILNG DATE: 2001-09-37

PRIOR PLILNG DATE: 2001-01-09

PRIOR PLILNG DATE: 2001-01-09

PRIOR PLILNG DATE: 2001-01-09

PRIOR PLILNG DATE: 2001-01-09

PRIOR PLILNG DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-01-09

PRIOR FILING DATE: 2001-01-09

PRIOR FILING DATE: 2001-01-30
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NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
RDBESSES: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: US
COMPUTER NEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/906,606
FILING DATE: 30-NO. US20020127653A1-2001
RPLICATION NUMBER: US/09/908,490
FILING DATE: 4UNKNOWN-
PRIORE/AGENTIN NUMBER: 36,688
REGISTRATION UNMBER: 36,688
REGISTRATION UNMBER: 36,688
REGISTRATION UNMBER: 36,688
REGISTRATION NUMBER: 36,688
REGISTRATION NUMBER: 36,688
REGISTRATION NUMBER: 31-260
INFORMATION: COND 371-260
INFORMATION FOR SEQ ID NO: 4:
CELEPAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 4:
CELEPAX: (202) 371-2540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: nucleic acid
; STRANDEDNESS: single
; POPOLOGY: linear
; MOLECULE TYPE: CDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-996-606-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3356 AGAGGAGGCGGCTGCGGGTCGTGGG 3380
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Patent No. US20020048800A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27 AGTGGAGGGGGGGGGGTCGACGG 3
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Gaps ö

Length 25; Indels

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Sequence 16, Application US/09804717A

Sequence 16, Application US/09804717A

Patent No. US20020164311A1

GENERAL INFORMATION:

APPLICANT: Strom, Terry B.

APPLICANT: Libermann, Towia

TITLE OF INVENTION: METHODS AND COMPOUNDS FOR PREVENTION OF GRAFT REJECTION

FILE REFERENCE: 01948-051003

CURRENT PILING DATE: 2002-04-25

PRIOR FILING DATE: 1999-05-04

PRIOR FILING DATE: 1999-05-04

PRIOR FILING DATE: 1999-05-04

PRIOR FILING DATE: 1999-05-04

PRIOR FILING DATE: 1993-03-01

PRIOR FILING DATE: 1993-03-01

PRIOR FILING DATE: 1993-03-01

PRIOR FILING DATE: 1992-02-28

NUMBER OF SEQ ID NOS: 46

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
APPLICANT: ROSENKRANDS, Ida
APPLICANT: WELDINGH, Karin
APPLICANT: FLORIO, Walter
TITLE OF INVENTION: NUCLEC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
TITLE OF INVENTION: NUCLEC ACIDS FRAGMENTS
FILE REFERENCE: 670001-2002.1
CURRENT APPLICATION NUMBER: US/09/791,171
CURRENT APPLICATION NUMBER: 09/050,739
PRIOR FILING DATE: 1998-03-30
PRIOR FILING DATE: 1997-04-02
PRIOR FILING DATE: 1997-04-02
PRIOR FILING DATE: 1997-04-04-02
PRIOR FILING DATE: 1997-04-18
PRIOR FILING DATE: 1998-01-05
NUMBER OF SEQ ID NOS: 173
SOFTWARE: PALENTIN VET: 2.0
SEQ ID NO 160

**LENGTH: NAMA
**LEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 0.4%; Score 17.4; DB 10; Best Local Similarity 77.8%; Pred. No. 3.4e+05; Matches 21; Conservative 0; Mismatches 6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA; ORGANISM: Mycobacterium tuberculosis
US-09-791-171-160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 TGAGATCTAGAATGCCACAGGGAACTG 28
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Matches 19; Conservative
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ORGANISM: Homo sapiens
US-09-804-717A-16
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US-09-866-108-3764
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Sequence 20, Application US/09894633A

Petent No. US20020124285A1

GENERAL INFORMATION:
APPLICANT: Conner, Timothy

APPLICANT: Obnofs, Patrice
APPLICANT: Malven, Marianne
APPLICANT: Malven, James

TITLE OF INVENTION: PLANT REGULATORY SEQUENCES FOR SELECTIVE CONTROL OF GENE EXPRESSI

TITLE OF INVENTION: PLANT REGULATORY WINBER: 06/214,357

FILE REFERENCE: 2000-06-28

PRIOR APPLICATION NUMBER: 60/214,357

PRIOR PAPLICATION NUMBER: 09/894,633

PRIOR PLING DATE: 2000-06-28

NUMBER OF SEQ ID NOS: 111

SEQ ID NO 20

LENGTH: 28

LENGTH: 28
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LOCATION: (1)..(28)

1 OTHER INFORMATION: synthetic primer sequence

US-09-894-6338-20
                 PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2001-09-21
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 15752
SEQ ID NO 3780
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Patent No. US20020043361
GENERAL INFORMATION:
APPLICANT: ANDERSEN, Peter
APPLICANT: NIELSEN, Rikke
APPLICANT: OFTINGER, Thomas
APPLICANT: RASMUSSEN, Peter Birk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2322 CCCAGACCAAGGAGCTGATGCACT 2345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 83.3
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Homo sapiens
US-09-866-108-3780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 5
US-09-894-633A-20/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
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TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
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APPLICANT: GU, YIZHONG
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: RANK, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
TITLE OF INVENTION: WYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
PILE REFERENCE: AEOMICA-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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80.0%; Pred. No. 3.9e+05;
tive 0; Mismatches 5;
                                           TILE REFERENCE: AEOMICA-7

CURRENT APPLICATION NUMBER: US/09/866,108

CURRENT FILING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR PELICATION NUMBER: US 60/207,456

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-09-27

PRIOR PELICATION NUMBER: US 60/236,359

PRIOR PILING DATE: 2000-09-27

PRIOR PELICATION NUMBER: PCT/US01/00666

PRIOR PILING DATE: 2001-01-30

PRIOR PELICATION NUMBER: PCT/US01/00667

PRIOR PELICATION NUMBER: PCT/US01/00669

PRIOR PELING DATE: 2001-01-30

PRIOR PELICATION NUMBER: PCT/US01/00669

PRIOR PELING DATE: 2001-01-30

PRIOR PELING DA
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CURRENT FILING DATE: 2001-05-25
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PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
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Patent No. US20020048800A1
GENERAL INFORMATION:
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Best Local Similarity 80.07
elthog 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Homo sapiens US-09-866-108-3778
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                                                                                          APPLICANT: GU, Yizhong
APPLICANT: GU, Yizhong
APPLICANT: GU, Yizhong
APPLICANT: BRN, Sharron G.
APPLICANT: BRN, David R.
APPLICANT: HANZEL, David R.
APPLICANT: HANZEL, David R.
APPLICANT: HANNON, Mark.
TILLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
FILE REFRENCE: ALGANICA-7
CURRENT APPLICATION NUMBER: US 60/207, 456
PRIOR APPLICATION NUMBER: US 60/207, 456
PRIOR APPLICATION NUMBER: US 60/207, 456
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US 60/236, 359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR PILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
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3.9e+05;
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PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2001-01-30
PRIOR PLING DATE: 2000-09-21
PRIOR PLING DATE: 2000-09-21
PRIOR PLING DATE: 2000-02-05
PRIOR PLING DATE: 2000-02-05
PRIOR PLING DATE: 2001-02-05
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SOFTWARE: Acomica Sequence Listing Engine
SEQ ID NO 3764
LENGTH: 25
Sequence 3764, Application US/09866108
Patent No. US20020048800A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3778, Application US/09866108
Patent No. US20020048800A1
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
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- JI, Yonggang
- PENN, Sharron G
- HANZEL, David K.
- RANK, David R.
- CHEN, Wensheng
- SHANNON, Mark
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                                                                            GENERAL INFORMATION:
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APPLICANT:
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APPLICANT:
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Matches
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Gaps

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APPLICANT: CHEN, WALK
TITLE OF INVENTION: MACSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
CURRENT APPLICATION UNMERR: US/09/866,108
CURRENT FILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PLICATION NUMBER: US 60/236,359
PRIOR PLICATION NUMBER: PCT/US01/00666
PRIOR PLING DATE: 2000-09-27
PRIOR PLING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR PLING DATE: 2001-01-30
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80.0%; Pred. No. 3.9e+05;
tive 0; Mismatches 5; Indels
PRIOR APPLICATION NUMBER: PCT/USO1/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00663
PRIOR APPLICATION NUMBER: PCT/USO1/00662
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2001-01-05
PRIOR FILING DATE: 2001-00-05
NUMBER OF SEQ ID NOS: 15752
SOFTWARE: ABOMICA SEQUENCE LISTING ENGINE
SEQ ID NO 3945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/USO1/00662
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/USO1/00661
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/USO1/00670
FILING DATE: 2001-01-30
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APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
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APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
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CORGANISM: Homo sapiens
US-09-866-108-3945
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Best Local Similarity
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US-09-866-108-4394
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US-09-866-108-3945

Sequence 3945, Application US/09866108

APPLICANT: Us vongang

APPLICANT: PENN, Sharron G.

APPLICANT: ENANK, David K.

APPLICANT: SHANNON, MAIK

TITLE OF INVENTION: WORSHER

TITLE OF INVENTION: WHOER: US/09/866,108

CURRENT APPLICATION NUMBER: US/09/866,108

CURRENT APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-00-04

PRIOR FILING DATE: 2000-00-04

PRIOR PELICATION NUMBER: US 60/236,359

PRIOR PELICATION NUMBER: PCT/US01/00666

PRIOR PPLICATION NUMBER: PCT/US01/00666

PRIOR PELICATION NUMBER: PCT/US01/00666

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR PLILATION NUMBER: PCT/US01/00669

PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR APPLICATION NUMBER: PCT/US01/00665

PRIOR PLILNG DATE: 2001-01-30

PRIOR PLILNG DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30
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              PRIOR APPLICATION NUMBER: PCT/USO1/00666
PRIOR FILING DATE: 2001-01-30
PRIOR PLLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00663
PRIOR PLLING DATE: 2001-01-30
PRIOR PLLING DATE: 2001-02-05
NUMBER OF SECI DA NOSS: 1575-1
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LENGTH: 25
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US-09-866-108-3895
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Length 25;

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Query Match 0.4%; Score 17; DB 10; L
Best Local Similarity 80.0%; Pred. No. 3.9e+05;
Matches 20; Conservative 0; Mismatches 5;
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; ORGANISM: Homo sapiens
US-09-866-108-12035
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Best Local Similarity
Matches 20; Conserv
              US-09-866-108-4395
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TITLE OF INVENTION: WYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT APPLICATION NUMBER: US/09/866,108
CURRENT FILING DATE: 2000-05-25
PRIOR PLICATION NUMBER: GB 24263.6
PRIOR PLICATION NUMBER: GB 24263.6
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR PLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR PLICATION NUMBER: PCT/US01/00666
PRIOR PLICATION NUMBER: PCT/US01/00666
PRIOR PLICATION NUMBER: PCT/US01/00669
PRIOR PLICATION NUMBER: PCT/US01/00661
PRIOR PLICATION NUMBER: PCT/US01/00661
PRIOR PLICATION NUMBER: US 60/234,687
PRIOR PLICATION NUMBER: US 60/236,860
PRIOR PLICATION NUMBER: US 60/226,860
PRIOR PLICATION NUMBER: US 60/236,860
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0.4%; Score 17; DB 10;
Best Local Similarity 80.0%; Pred. No. 3.9e+05;
Matches 20; Conservative 0; Mismatches 5
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/266,860
PRIOR FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 15752
SOFTWARR: Aeomica Sequence Listing Engine
SEQ ID NO 4394
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-866-108-4395
; Sequence 4395, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
APPLICANT: GI, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
APPLICANT: HANZEL, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  653 CGCCGCCAGCAGCTGGGCTGGGAGG 677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CGCCAGCAGCTCCTGGGAAGGGAAG 25
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ORGANISM: Homo sapiens
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; ORGANISM: Homo sapiens
US-09-866-108-4394
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APPLICANT: RANK, DAVIG R.
APPLICANT: RANK, DAVIG R.
APPLICANT: GHEN, Wesheng
APPLICANT: GHEN, WESHENG
APPLICANT: GHEN, WESHENG
APPLICANT: GHEN, WESHENG
APPLICANT: GHANNON, MATK
TITLE REPRENCE: ADONICA-7
CURRENT APPLICATION UNDER: US/09/866,108
CURRENT APPLICATION UNDER: US/09/866,108
CURRENT APPLICATION UNDER: US/09/866,108
REIOR APPLICATION NUMBER: US/02/3,456
REIOR APPLICATION NUMBER: PC/02/3,456
REIOR APPLICATION NUMBER: PC/02/3,456
REIOR APPLICATION NUMBER: PC/02/3,459
REIOR FILING DATE: 2000-09-27
REIOR APPLICATION NUMBER: PC/USO1/0066
REIOR FILING DATE: 2001-01-30
REIOR FILING DATE: 2001-01-30
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80.0%; Pred. No. 3.9e+05;
iive 0; Mismatches 5;
Sequence 12035, Application US/09866108 Patent No. US20020048800A1
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Search completed: March 4, 2003, 06:46:21 Job time : 1106 secs

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AA973948 oq12d02.8
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AZ404206 IM0172120
AZ788420 ZM0136M06
AA953755 om899b03.8
BM398127 5009-0-18
AZ342274 IM0076C04
AZ601864 IM0420P16
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BH810436 SALK\_0495
AZ36810 IM003623
AZ37811 IM0079816
AZ308159 IM0010009
AZ368069 IM0013623
AZ45533 IM0079816
AZ405312 UA70803 .r
AZ8032508 ZM0018C24
AZ368062 ZM0036409
AZ8032508 ZM0037813
AZ622508 ZM0027807
AZ942905 ZM0027807
AZ942905 ZM0027807
AZ6242965 .x
AI652325 ZM0027807

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Homosapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Hosses; Lo 28)

Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,

K., Hillier, L., Cannon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,

Chissoe, S., Dietrich, M., Dubuque, T., Ravello, A., Gish, M., Hawkins

M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E.,

B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T.,

Schellenberg, K., Soares, M.B., Tan, F., Thlerry-Wag, J., Trevaskis, E.,

Generation and analysis of 280,000 human expressed sequence tags

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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H41620
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AZ779573
BA4016118
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VERSION
KEYWORDS
SOURCE
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JOURNAL
MEDLINE
COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT T47368
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BM399411 5009-0-57
ALS84657 ALS84657
BH861248 SALK_0678
AA479681 1M0300G02
AZ780072 ZM0017H04
                                                                                                                            3, 2003, 19:51:57 ; Search time 4726 Seconds (without alignments) 13255.214 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                      30108
                     GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                   16154066 segs, 8097743376 residues
                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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AL584657
BH861248
AZ479681
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                                                                                             nucleic search, using sw model
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em_est5m:*
em_est6m:*
gb_ss:*
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Match Length
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Post-processing:

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Indels

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SALK_067873 Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_067873, DNA sequence.
BH861248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AL584657 28 bp mRNA linear EST 28-FEB-2001 AL584657 Stratagene Chick Embryo Lambda cDNA Library (* 937405) Gallus gallus CDNA clone ROS012G12, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                       Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 28)
Murray, F.
                                                                                                                                                                                                                                                                                                                                Stratagene Chick Embryo Lambda cDNA Library
Unpublished (2001)
Contact: Frazer Murray
 Pred. No. 5.9e+06;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.5%; Score 18; DB 9; Le
100.0%; Pred. No. 7.8e+06;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                            Dept. Genomics and Bioinformatics Roslin institute
Roslin, Midlothian, EH25 9PS, UK
Tel: +44 (0)131 527 4200
Fax: 44 (0)131 440 0434
Email: frazer murray@bsrc.ac.uk
Seq primer: T3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .28
/organism="Gallus gallus"
/db_xref="taxon:9031"
/clone="ROS012G12"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                          AL584657.1 GI:13163388
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 84.08;
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ORIGIN
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TITLE
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AL584657
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EST 17-JAN-2002
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Pred. No. 3.4e+06;
0; Mismatches 4; Indels
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                                                                                                                   High quality sequence stop: 1. Location/Qualifiers
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 est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 CGAGCGGGTCAAGCTGCTGCTGCAGG 27
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Tetrahymena thermophila
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1 Similarity 84.6%;
22; Conservative
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Length 28;

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Ouery Match 0.4
Best Local Similarity 90.0
Matches 18; Conservative
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AZ780072
                                            FEATURES
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              L (Dasses I.C. 23)

S. Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J. and Ecker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
Inpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker(salk.edu
This is single pass sequence recovered from the left border of This is single pass sequence lies within an annotated intron of At5940020.
Class: TDNA tagged.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AZ479681 25 bp DNA linear GSS 04-OCT-2000 1M0300G02R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0300G02 R, DNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:3702"
/clone="SALK_067873"
/clone="SALK_067873"
/clone="Ibb" Arabidopsis thaliana TDNA insertion lines force="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
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80.0%; Pred. No. 1.3e+07;
Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Arabidopsis thaliana"/strain="Columbia 0"
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Insert Length: 10000 Std Error: 0.00
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Seg primer: CACACAGGAAACAGCTATGACC
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Fax: 801 585 7177
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es 20; Conserv
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84112, USA
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/note="Vector: Distrain Ally vold, ill.resisant, FT"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G57BL/60 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jar.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil472214|gb|RF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was ennealed to
adaptored vector DNA, and transformed into
chemically-competent E. coll XL10-Gold (Stratagene) cells
and selected for ampletillin resistance."
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Nalan, H., Longacres, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
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                                                                                                                          /strain="C57BL/6J"
/db_xref="taxon:10090"
/dclone="tuuccim0300G02"
/clone_lib="mouse 10kb plasmid UUGCIM library"
/sex="Male"
/lab_host="E. Coli strain XLI0-Gold, Ti-resistant,
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
lnsert Length: 10000 Std Error: 0.00
Plate: 0017 row: H column: 04
Seq primer: CGTTGTAAAACGACGCCAGT
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                    /organism-"Mus musculus"
High quality sequence stop: 26.
Location/Qualifiers
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us-10-049-743-1.lim30.rst

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/ Colone—"Lib—"Homo sapiens"
// Corganism="Homo sapiens"
// Colone—"Lib—"Nor_Cosp_cosp_"
// Colone—"Lib—"Nor_Cosp_cosp_"
// Colone—"Lib—"Nor_Cosp_cosp_"
// Lissue_type="pooled germ cell tumors"
// Lab_host="PHIOB"
// Lab_host=
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1 (bases 1 to 30)

Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E., Frankel

7. and Klobutcher,L.

5.7 and Klobutcher,L.

6.002)

Unpublished (2002)

Contact: Turkewitz AP

Molecular Genetics and Cell Biology

University of Chicago

University of Chicago, IL 60637, USA
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/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: BlueScript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."
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Eukaryota, Alveolata, Ciliophora, Oligohymenophorea,
Hymenostomatida, Tetrahymenina, Tetrahymena.
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    .30
    /organism="Tetrahymena thermophila"
/strain="CU428.1"

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75.0%; Pred. No. 1.5e+07;
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0.4%; Score 16.8; DB 9;
Best Local Similarity 75.0%; Pred. No. 1.5e+07;
Matches 21; Conservative 0; Mismatches 7;
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
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Seq primer: T3.
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Best Local Similarity 75.09
Matches 21; Conservative
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Fax: 773 702 3172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BASE COUNT
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BM398517
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CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCICARP Clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EST 23-JUL-1998
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Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
Eukaryota, Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA973948 23-JUL-1
oq12d02.s1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1586115 3'
similar to TR:035787 035787 KINESIN-RELATED PROTEIN. ;, mRNA
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                          /sex="Male"
/lab_host="B. Coli strain XL10-Gold, T1-resistant, F-"
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 0.4%; Score 16.8; DB 17; Length 26; Best Local Similarity 90.0%; Pred. No. 1.4e+07; Matches 18; Conservative 0; Mismatches 2; Indels
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                                                                                                                                                      /organism="Mus musculus"
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/db_xref="taxon:10090"
/clone="UUGC2M0017H04"
          Class: plasmid enas
High quality sequence stop: 26.
Location/Qualifiers
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AA973948.1 GI:3149128
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Unpublished (1997)
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SOURCE

REFERENCE AUTHORS

JOURNAL COMMENT

TITLE

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/sex_mate.
/sex_mate.
/sex_mate.
/sex_mate.
/sex_mate.
/note="vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (mate) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.055 inch orifice at constant velocity. The sheared DNA
was blunt end repaired with 74 DNA polymerase and 74
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil473214)gplAR129072.1), a copy number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chamically-competent E. coll XL10-Gold (Stratagene) cells
and selected for ampicillar resistance.

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                                                                                                                                                                     AZ789420 2M0037J11F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0037J11 F, DNA sequence.
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Butaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bunanjota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 29)

Dunn, D., Aoyaqi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
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/db_cref="texon:10090"
/clone="UGCZM0037J11"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/sex="Male"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0037 row: J column: 11
Seg primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
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Location/Qualifiers
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       1 CTGCTGCTGCTGCTGCTGCT 23
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//ab_host="E. Coli strain XIIO-Gold, Tl-resistant, F-"
//ab_host="E. Coli strain XIIO-Gold, Tl-resistant, F-"
//note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G75BL/GJ (male) was obtained from the Jackson
Laboratory Mouse DNA Resources
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
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was blunt end-repaired with T4 DNA polymerase and T4
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adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil4/32114 gplA129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
chemically-competent E. coli XLLO-Gold (Stratagene) cells
and selected for ampicillin resistance. "tratagene) cells
                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Sclurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 27)

E Junn, D., Aoyaji, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, Rose and Reads from 10kb plasmid inserts
Unpublished (2000)

L Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
RM. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                                                                                           A2404206 27 bp DNA linear GSS 03-OCT-2000 1M0172120F Mouse 10kb plasmid UUGClM library Mus musculus genomic clone UUGCLM0172120 F, DNA sequence.
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/organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: ddunnegenetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 01/2 row: I column: 20
Seg primer: cGTTGTAAAACGACGCCAGT
Class: plasmid ends
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3 CTGAGCTCACGCGGGGGGGCCCGGTACC 30
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Fax: 801 585 7177
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1...22
/organism="Homo sapiens"
/organism="Homo sapiens"
/do_xref="tsoares_NFL_T_GBC_S1"
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                                                                                                                                                                                                                                                                                               30 bp mRNA linear EST 17-JAN-2002 5000-0-41-A08.t.1 Chilcoat/Turkewitz cDNA (large fraction)
Extrahymena thermophila cDNA, mRNA sequence.
BM398127 GI:18198180
EST.
                                                                                                                    EST 23-JUN-1998
                                                                                                                    AA953755 23-JUN-199
on89b03.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
IMAGE:1563821 3' similar to TR:Q92759 Q92759 TRANSCRIPTION FACTOR
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Tetrahymena thermophila
Bukaryota, Alveolata, Ciliophora; Oligohymenophorea;
Hymenostomatida: Tetrahymenina; Tetrahymena.
1 (bases 1 to 30)
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  4 CACACTGCCAGTTCTTGTACAGGTGC 29
                                                                                                                                                                                       AA953755
AA953755 GI:3116673
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BM398127/c
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AA953755/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
RAI 12, USA
RAI 12, USA
Tel: 801 885 5606
Fax: 801 585 7177
                                                                                                                  A2840149 30 bp DNA linear GSS 20-FEB-2001
2M0136M06R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC2M0136M06 R, DNA sequence.
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Relly, M., Rose, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /lab_host="E. Coli strain XLIO-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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/db_orge="taxon:10090"
/clone="taxon:10000"
/clone_lib="Mouse lOkb plasmid UUGCIM library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0136 row: M column: 06
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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26 AGTITAAGGAIGCAGICCAICAGAGC
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacze,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts.
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/db_xref="taxon:591"
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proc. Natl. Acad. Sci USA, 98: 8709-8713."
Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E., Frankel, J. and Klobutcher,L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells Onpublished (2002)
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Fax: 773 702 4373
Email: apturkew@midway.uchicago.edu
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/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 0.4%; Score 16.2; DB 13; Length 30; Best Local Similarity 72.4%; Pred. No. 2e+07; Matches 21; Conservative 0; Mismatches 8; Indels
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Fax: 801 585 7177
Email: ddunnegenetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0076 row: C column: 04
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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                                                                                                                                                                                                                              Seq primer: T3.
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Mus musculus
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with 74 DNA polymerase and 74 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarcse gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil473214/gblAR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coll XL10-Gold (Stratagene) cells and selected for ampicilia resistance."
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AZ601864 GI:11724054
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/note="Vector: PWD42Nry Purified genomic DNA from M.
musculus (57BL/G) (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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/clone="taxon:10x010 | clone_lib="Mouse 10xb plasmid UUGCIM library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 0.4%; Score 16.2; DB 17; Length 30; 11 Similarity 72.4%; Pred. No. 2e+07; 21; Conservative 0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0420 row: P column: 16
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasnid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1088 AAACCGCGTGCCAAACCACCTCCCATTCC 1116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence stop: 30.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30 AACCCAGGTGCCATACCAGCACTCATACC 2
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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/61 (male) was obtained from the Jackson
laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide Kinase. Adaptor oligonocleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil472114) gip|par129072.11, a copy.number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for amploilla resistance."
8 a
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ORIGIN
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29 TGTCCCATGCATCCTATCAAACCACCATG 1 g

2983 TGTCCCATTCATCCTCACCTACGACTTTG 3011

δ

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Gaps 0;

Query Match 0.4%; Score 16.2; DB 17; Length 30; Best Local Similarity 72.4%; Pred. No. 2e+07; Matches 21; Conservative 0; Mismatches 8; Indels (

Search completed: March 4, 2003, 06:25:19 Job time: 4732 secs